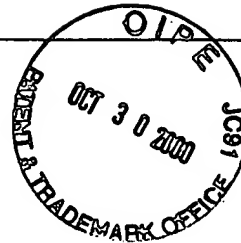


SEQUENCE LISTING



RECEIVED

NOV 06 2000

TECH CENTER 1600/2000

<110> DALY, Roger J.
SUTHERLAND, Robert L.

<120> A Potential Effector for the Grb7 Family of Signalling
Proteins

<130> 1871-129

<140> 09/509,196

<141> 2000-03-23

<150> P09388

<151> 1997-09-23

<150> PCT AU98/00795

<151> 1998-09-23

<160> 2

<170> PatentIn Ver. 2.1

<210> 1

<211> 3400

<212> DNA

<213> Homo sapiens

<400> 1

attcctcttc ataatgcatg ctcttttggg catgctgaag tagtcaatct ccttttgcca 60
catggtgcag accccaatgc tcgagataat tggaattata ctctctcca tgaagctgca 120
attaaaggaa agattgatgt ttgcattgtg ctgttacagc atggagctga gccaaccatc 180
cgaaatacag atggaaggac agcattggat ttagcagatc catctgccaa agcagtgtct 240
actggtgaat ataagaaaga tgaactctta gaaagtgccg ggagtggcaa tgaagaaaaa 300
atgatggctc tactcacacc attaaatgtc aactgccacg caagtgatgg cagaaagtca 360
actccattac atttggcagc aggatataac agagtaaaga ttgtacagct gttactgcaa 420
catggacgtg atgtccatgc taaagataaa ggtgatctgg taccattaca caatgcctgt 480
tcttatggctc attatgaagt aactgaactt ttggtcaagc atggtggctg tgtaaatgca 540
atggacttgt ggcaattcac tcctcttcat gaggcagctt ctaagaacag ggttgaagta 600
tgttctcttc tcttaagtta tgggtgcagac ccaacactgc tcaattgtaa gaataaaagt 660
gctatagact tggctccac accacagtta aaagaaagat tagcatatga atttaaaggc 720
cactcggtgc tgcaagctgc acgagaagct gatgttactc gaatcaaaaa acatctctct 780
ctggaaatgg tgaatttcaa gcatcctcaa acacatgaaa cagcattgca ttgtgctgct 840
gcatctccat atcccaaaag aaagcaaata tgtgaactgt tgctaagaaa aggagcaaac 900
atcaatgaaa agactaaaga attcttgact cctctgcacg tggcatctga gaaagctcat 960
aatgatgttg ttgaagtagt ggtgaaacat gaagcaaagg ttaatgctct ggataatctt 1020
ggtcagactt ctctacacag agctgcatat tgtggtcatc tacaaacctg ccgcctactc 1080
ctgagctatg ggtgtgatcc taacattata tcccttcagg gctttactgc tttacagatg 1140

RECEIVED

NOV 01 2000

TECH CENTER 1600/2000

```

ggaaatgaaa atgtacagca actcctccaa gagggatatct cattaggtaa ttcagaggca 1200
gacagacaat tgctggaagc tgcaaaggct ggagatgtcg aaactgtaaa aaaactgtgt 1260
actgttcaga gtgtcaactg cagagacatt gaagggcgtc agtctacacc acttcatttt 1320
gcagctgggt ataacagagt gtccgtggtg gaatatctgc tacagcatgg agctgatgtg 1380
catgctaaag ataaaggagg ccttgtagct ttgcacaatg catgttctta cggacattat 1440
gaagttgcag aacttcttgt taaacatgga gcagtagtta atgtagctga tttatggaaa 1500
tttacacctt tacatgaagc agcagcaaaa ggaaaatatg aaatttgcaa acttctgctc 1560
cagcatgggt cagaccctac aaaaaaaaaa agggatggaa atactccttt ggatcttggt 1620
aaagatggag atacagatat tcaagatctg cttaggggag atgcagcttt gctagatgct 1680
gccagaagg gttgttttagc cagagtgaag aagttgtctt ctctgataa tgtaaattgc 1740
cgcgataccc aaggcagaca ttcaacacct ttacatttag cagctgggta taataattta 1800
gaagttgcag agtatttggt acaacacgga gctgatgtga atgccaaga caaaggagga 1860
cttattcctt tacataatgc agcatcttac gggcatgtag atgtagcagc tctactaata 1920
aagtataatg catctctcaa tgccacggac aaatgggctt tcacaccttt gcacgaagca 1980
gcccaaaagg gacgaacaca gctttgtgct ttgttgctag cccatggagc tgacccgact 2040
cttaaaaatc aggaaggaca aacaccttta gatttagttt cagcagatga tgtcagcgct 2100
cttctgacag cagccatgcc cccatctgct ctgccctctt gttacaagcc tcaagtgtc 2160
aatgggtgta gaagcccagg agccactgca gatgctctct cttcagggtc atctagccca 2220
tcaagccttt ctgcagccag cagtcttgac aacttatctg ggagtttttc agaactgtct 2280
tcagtagtta gttcaagtgg aacagagggt gcttccagtt tggagaaaaa ggaggttcca 2340
ggagtagatt ttagcataac tcaattcgta aggaatcttg gacttgagca cctaattgat 2400
atatttgaga gagaacagat cactttggat gtattagttg agatggggca caaggagctg 2460
aaggagattg gaatcaatgc ttatggacat aggcacaaaac taattaaagg agtcgagaga 2520
cttatctccg gacaacaagg tcttaacca tatttaactt tgaacacctc tggtagtgga 2580
acaattctta tagatctgtc tctgatgat aaagagtttc agtctgtgga ggaagagatg 2640
caaagtacag ttcgagagca cagagatgga ggtcatgcag gtggaatctt caacagatac 2700
aatattctca agattcagaa ggtttgtaac aagaaactat gggaaagata cactcaccgg 2760
agaaaagaag tttctgaaga aaaccacaac catgccaatg aacgaatgct atttcatggg 2820
tctccttttg tgaatgcaat tatccacaaa ggctttgatg aaaggcatgc gtacataggt 2880
ggtagtgggt gagctggcat ttattttgct gaaaactctt ccaaaagcaa tcaatatgta 2940
tatggaattg gaggaggtac tgggtgtcca gttcacaaaag acagatcttg ttacatttgc 3000
cacaggcagc tgctcttttg ccgggtaacc ttgggaaagt ctttctgca gttcagtgc 3060
atgaaaatgg cacattctcc tccaggtcat cactcagtca ctggtaggcc cagtgtaaat 3120
ggcctagcat tagctgaata tgttatttac agaggagaac aggccttatcc tgagtattta 3180
attacttacc agattatgag gcctgaagggt atggtcgatg gataaatagt tattttaaga 3240
aactaattcc actgaacctt aaatcatcaa agcagcagtg gcctctacgt ttactcctt 3300
tgctgaaaaa aaatcatctt gccacaggc ctgtggcaaa aggataaaaa tgtgaacgaa 3360
gtttaacatt ctgacttgat aaagctttaa taatgtacag 3400

```

```

<210> 2
<211> 1074
<212> PRT
<213> Homo sapiens

```

```

<400> 2
Ile Pro Leu His Asn Ala Cys Ser Phe Gly His Ala Glu Val Val Asn
1 5 10 15

```

Leu	Leu	Leu	Arg	His	Gly	Ala	Asp	Pro	Asn	Ala	Arg	Asp	Asn	Trp	Asn		
			20					25					30				
Tyr	Thr	Pro	Leu	His	Glu	Ala	Ala	Ile	Lys	Gly	Lys	Ile	Asp	Val	Cys		
		35					40					45					
Ile	Val	Leu	Leu	Gln	His	Gly	Ala	Glu	Pro	Thr	Ile	Arg	Asn	Thr	Asp		
	50					55					60						
Gly	Arg	Thr	Ala	Leu	Asp	Leu	Ala	Asp	Pro	Ser	Ala	Lys	Ala	Val	Leu		
65					70					75					80		
Thr	Gly	Glu	Tyr	Lys	Lys	Asp	Glu	Leu	Leu	Glu	Ser	Ala	Arg	Ser	Gly		
				85				90						95			
Asn	Glu	Glu	Lys	Met	Met	Ala	Leu	Leu	Thr	Pro	Leu	Asn	Val	Asn	Cys		
			100					105					110				
His	Ala	Ser	Asp	Gly	Arg	Lys	Ser	Thr	Pro	Leu	His	Leu	Ala	Ala	Gly		
		115					120					125					
Tyr	Asn	Arg	Val	Lys	Ile	Val	Gln	Leu	Leu	Leu	Gln	His	Gly	Arg	Asp		
	130						135				140						
Val	His	Ala	Lys	Asp	Lys	Gly	Asp	Leu	Val	Pro	Leu	His	Asn	Ala	Cys		
145					150					155					160		
Ser	Tyr	Gly	His	Tyr	Glu	Val	Thr	Glu	Leu	Leu	Val	Lys	His	Gly	Gly		
				165					170					175			
Cys	Val	Asn	Ala	Met	Asp	Leu	Trp	Gln	Phe	Thr	Pro	Leu	His	Glu	Ala		
			180					185					190				
Ala	Ser	Lys	Asn	Arg	Val	Glu	Val	Cys	Ser	Leu	Leu	Leu	Ser	Tyr	Gly		
		195					200					205					
Ala	Asp	Pro	Thr	Leu	Leu	Asn	Cys	Lys	Asn	Lys	Ser	Ala	Ile	Asp	Leu		
	210					215					220						
Ala	Pro	Thr	Pro	Gln	Leu	Lys	Glu	Arg	Leu	Ala	Tyr	Glu	Phe	Lys	Gly		
225					230					235					240		
His	Ser	Leu	Leu	Gln	Ala	Ala	Arg	Glu	Ala	Asp	Val	Thr	Arg	Ile	Lys		
				245					250					255			
Lys	His	Leu	Ser	Leu	Glu	Met	Val	Asn	Phe	Lys	His	Pro	Gln	Thr	His		
		260						265					270				

Glu Thr Ala Leu His Cys Ala Ala Ala Ser Pro Tyr Pro Lys Arg Lys			
275	280	285	
Gln Ile Cys Glu Leu Leu Leu Arg Lys Gly Ala Asn Ile Asn Glu Lys			
290	295	300	
Thr Lys Glu Phe Leu Thr Pro Leu His Val Ala Ser Glu Lys Ala His			
305	310	315	320
Asn Asp Val Val Glu Val Val Val Lys His Glu Ala Lys Val Asn Ala			
325	330	335	
Leu Asp Asn Leu Gly Gln Thr Ser Leu His Arg Ala Ala Tyr Cys Gly			
340	345	350	
His Leu Gln Thr Cys Arg Leu Leu Leu Ser Tyr Gly Cys Asp Pro Asn			
355	360	365	
Ile Ile Ser Leu Gln Gly Phe Thr Ala Leu Gln Met Gly Asn Glu Asn			
370	375	380	
Val Gln Gln Leu Leu Gln Glu Gly Ile Ser Leu Gly Asn Ser Glu Ala			
385	390	395	400
Asp Arg Gln Leu Leu Glu Ala Ala Lys Ala Gly Asp Val Glu Thr Val			
405	410	415	
Lys Lys Leu Cys Thr Val Gln Ser Val Asn Cys Arg Asp Ile Glu Gly			
420	425	430	
Arg Gln Ser Thr Pro Leu His Phe Ala Ala Gly Tyr Asn Arg Val Ser			
435	440	445	
Val Val Glu Tyr Leu Leu Gln His Gly Ala Asp Val His Ala Lys Asp			
450	455	460	
Lys Gly Gly Leu Val Pro Leu His Asn Ala Cys Ser Tyr Gly His Tyr			
465	470	475	480
Glu Val Ala Glu Leu Leu Val Lys His Gly Ala Val Val Asn Val Ala			
485	490	495	
Asp Leu Trp Lys Phe Thr Pro Leu His Glu Ala Ala Ala Lys Gly Lys			
500	505	510	
Tyr Glu Ile Cys Lys Leu Leu Leu Gln His Gly Ala Asp Pro Thr Lys			
515	520	525	

Lys Asn Arg Asp Gly Asn Thr Pro Leu Asp Leu Val Lys Asp Gly Asp
 530 535 540

Thr Asp Ile Gln Asp Leu Leu Arg Gly Asp Ala Ala Leu Leu Asp Ala
 545 550 555 560

Ala Lys Lys Gly Cys Leu Ala Arg Val Lys Lys Leu Ser Ser Pro Asp
 565 570 575

Asn Val Asn Cys Arg Asp Thr Gln Gly Arg His Ser Thr Pro Leu His
 580 585 590

Leu Ala Ala Gly Tyr Asn Asn Leu Glu Val Ala Glu Tyr Leu Leu Gln
 595 600 605

His Gly Ala Asp Val Asn Ala Gln Asp Lys Gly Gly Leu Ile Pro Leu
 610 615 620

His Asn Ala Ala Ser Tyr Gly His Val Asp Val Ala Ala Leu Leu Ile
 625 630 635 640

Lys Tyr Asn Ala Ser Leu Asn Ala Thr Asp Lys Trp Ala Phe Thr Pro
 645 650 655

Leu His Glu Ala Ala Gln Lys Gly Arg Thr Gln Leu Cys Ala Leu Leu
 660 665 670

Leu Ala His Gly Ala Asp Pro Thr Leu Lys Asn Gln Glu Gly Gln Thr
 675 680 685

Pro Leu Asp Leu Val Ser Ala Asp Asp Val Ser Ala Leu Leu Thr Ala
 690 695 700

Ala Met Pro Pro Ser Ala Leu Pro Ser Cys Tyr Lys Pro Gln Val Leu
 705 710 715 720

Asn Gly Val Arg Ser Pro Gly Ala Thr Ala Asp Ala Leu Ser Ser Gly
 725 730 735

Pro Ser Ser Pro Ser Ser Leu Ser Ala Ala Ser Ser Leu Asp Asn Leu
 740 745 750

Ser Gly Ser Phe Ser Glu Leu Ser Ser Val Val Ser Ser Ser Gly Thr
 755 760 765

Glu Gly Ala Ser Ser Leu Glu Lys Lys Glu Val Pro Gly Val Asp Phe
 770 775 780

Ser Ile Thr Gln Phe Val Arg Asn Leu Gly Leu Glu His Leu Met Asp
785 790 795 800

Ile Phe Glu Arg Glu Gln Ile Thr Leu Asp Val Leu Val Glu Met Gly
805 810 815

His Lys Glu Leu Lys Glu Ile Gly Ile Asn Ala Tyr Gly His Arg His
820 825 830

Lys Leu Ile Lys Gly Val Glu Arg Leu Ile Ser Gly Gln Gln Gly Leu
835 840 845

Asn Pro Tyr Leu Thr Leu Asn Thr Ser Gly Ser Gly Thr Ile Leu Ile
850 855 860

Asp Leu Ser Pro Asp Asp Lys Glu Phe Gln Ser Val Glu Glu Glu Met
865 870 875 880

Gln Ser Thr Val Arg Glu His Arg Asp Gly Gly His Ala Gly Gly Ile
885 890 895

Phe Asn Arg Tyr Asn Ile Leu Lys Ile Gln Lys Val Cys Asn Lys Lys
900 905 910

Leu Trp Glu Arg Tyr Thr His Arg Arg Lys Glu Val Ser Glu Glu Asn
915 920 925

His Asn His Ala Asn Glu Arg Met Leu Phe His Gly Ser Pro Phe Val
930 935 940

Asn Ala Ile Ile His Lys Gly Phe Asp Glu Arg His Ala Tyr Ile Gly
945 950 955 960

Gly Met Phe Gly Ala Gly Ile Tyr Phe Ala Glu Asn Ser Ser Lys Ser
965 970 975

Asn Gln Tyr Val Tyr Gly Ile Gly Gly Gly Thr Gly Cys Pro Val His
980 985 990

Lys Asp Arg Ser Cys Tyr Ile Cys His Arg Gln Leu Leu Phe Cys Arg
995 1000 1005

Val Thr Leu Gly Lys Ser Phe Leu Gln Phe Ser Ala Met Lys Met Ala
1010 1015 1020

His Ser Pro Pro Gly His His Ser Val Thr Gly Arg Pro Ser Val Asn
1025 1030 1035 1040

Gly Leu Ala Leu Ala Glu Tyr Val Ile Tyr Arg Gly Glu Glu Ala Tyr
1045 1050 1055

Pro Glu Tyr Leu Ile Thr Tyr Gln Ile Met Arg Pro Glu Gly Met Val
1060 1065 1070

Asp Gly

B1

